**WE CLAIM:**

1. A method for identifying tumor characteristics comprising:

measuring a copy number of at least two genes associated with lipid metabolism, synthesis, or action in cells of a patient tissue sample and comparing the results with a copy number in a normal cell.

2. The method of claim 1, wherein at least two of the genes associated with lipid metabolism, synthesis, or action are selected from the group consisting of: Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Dihydroxyacetone phosphate acyltransferase, Phosphate cytidylyltransferase 1 (choline specific, alpha form), Phosphate cytidylyltransferase 2 (ethanolamine specific), Phosphatidic Acid Phosphatase type 2c, Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase C beta 3 (phosphatidylinositol specific), Phosphatidylinositol-3-Kinase (class2, gamma polypeptide), Choline/ethanolamine phosphotransferase, Lyosphospholipase, Aldehyde dehydrogenase (5 family, member A1), Phospholipase D1 glycosylphosphatidylinositol specific, 1-acylglycerol-3-phosphate acyltransferase, Phosphatidic Acid Phosphate type 2b, Edg 1, Glycerol-3-phosphate dehydrogenase, Sphingosine-1-phosphate lyase 1, Phosphatase and Tenson Homolog (PTEN), Phosphatidic Acid Phosphatase type 2a, Sphingomyelin phosphodiesterase 1, N-acylsphingosine amidohydrolase, Glycerol Kinase, Diacylglycerol Kinase gamma, Acyl-dihydroxyacetone phosphate reductase, Triacylglycerol lipase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

3. The method of claim 1, wherein at least one of the genes associated with lipid metabolism, synthesis, or action is selected from the group consisting of Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase D1 glycosylphosphatidylinositol specific, Edg 1, Glycerol-3-phosphate dehydrogenase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

4. The method of claim 1, wherein the determination of the copy number of the genes associated with lipid metabolism, synthesis, or action is made by:

isolating sample nucleic acid polymers from cells of the patient tissue sample;

hybridizing the sample nucleic acid polymers with nucleic acid polymers specific for the selected genes to quantify the extent of hybridization; and

comparing the hybridization data thus obtained with data obtained from the hybridization of reference nucleic acid polymers isolated from a normal cell of the same tissue type as the patient tissue sample.

5. The method of claim 4, wherein the sample nucleic acid polymer in the isolating step is amplified by a polymerase chain reaction (PCR).

6. The method of claim 4, wherein the step of hybridizing the sample nucleic acid polymers uses a nucleic acid polymer comprising at least about 19 nucleotides to hybridize to a coding region of one of the selected genes.

7. The method of claim 4, wherein the step of hybridizing the sample nucleic acid polymers uses a nucleic acid polymer comprising at least about 19 nucleotides to hybridize to a non-coding sequence functionally linked to the coding region of one of the selected genes, and wherein the non-coding functionally linked sequence is unique to that gene.

8. The method of claim 4, wherein the hybridizing step uses nucleic acid polymers specific for the selected genes that are immobilized on a solid support wherein a nucleic acid polymer specific for each selected gene is located at a predetermined position on the solid support.

9. A method for identifying tumor characteristics comprising measuring the expression level of at least two genes associated with lipid metabolism, synthesis, or action in a patient tissue sample and comparing the results with an expression level in normal cells.

10. The method of claim 9, wherein at least two of the genes associated with lipid metabolism, synthesis, or action are selected from the group consisting of: Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Dihydroxyacetone phosphate acyltransferase, Phosphate cytidylyltransferase 1 (choline specific, alpha form), Phosphate cytidylyltransferase 2 (ethanolamine specific), Phosphatidic Acid Phosphatase type 2c, Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase C beta 3 (phosphatidylinositol specific), Phosphatidylinositol-3-Kinase (class2, gamma polypeptide), Choline/ethanolamine phosphotransferase, Lyosphospholipase,

Aldehyde dehydrogenase (5 family, member A1), Phospholipase D1 glycosylphosphatidylinositol specific, 1-acylglycerol-3-phosphate acyltransferase, Phosphatidic Acid Phosphate type 2b, Edg 1, Glycerol-3-phosphate dehydrogenase, Sphingosine-1-phosphate lyase 1, Phosphatase and Tenson Homolog (PTEN), Phosphatidic Acid Phosphatase type 2a, Sphingomyelin phosphodiesterase 1, N-acylsphingosine amidohydrolase, Glycerol Kinase, Diacylglycerol Kinase gamma, Acyl-dihydroxyacetone phosphate reductase, Triacylglycerol lipase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

11. The method of claim 9, wherein at least one of the genes associated with lipid metabolism, synthesis, or action is selected from the group consisting of Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase D1 glycosylphosphatidylinositol specific, Edg 1, Glycerol-3-phosphate dehydrogenase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

12. The method of claim 9, wherein the determination of the expression level of the genes associated with lipid metabolism, synthesis, or action is made by:

isolating sample ribonucleic acid polymers from the cells of the patient tissue sample;

hybridizing the sample ribonucleic acid polymers with nucleic acid polymers specific for the selected genes to quantify the extent of hybridization; and

comparing the hybridization data thus obtained with data obtained from the hybridization of reference nucleic acid polymers isolated from a normal cell of the same tissue type as the patient tissue sample.

13. The method of claim 12, wherein the sample ribonucleic acid polymer in the isolating step is amplified by a polymerase chain reaction (PCR) technique.

14. The method of claim 12, wherein the step of hybridizing the sample ribonucleic acid polymers uses a nucleic acid polymer comprising at least about 19 nucleotides to hybridize to a coding region of one of the selected genes.

15. The method of claim 12, wherein the step of hybridizing the sample ribonucleic acid polymers uses a nucleic acid polymer comprising at least about 19 nucleotides to hybridize to a non-coding sequence functionally linked to the coding region of one of the selected genes, wherein the functionally linked non-coding sequence is unique to that gene.

16. The method of claim 12, wherein the hybridizing step uses nucleic acid polymers specific for the selected genes that are immobilized on a solid support wherein a nucleic acid polymer specific for each selected gene is located at a predetermined position on the solid support.

17. A physical platform comprising an array of nucleic acid polymers immobilized at a predetermined position on a solid support:

wherein the array is comprised of at least two different isolated nucleic acid polymers which are each specific for a different gene associated with lipid metabolism, synthesis, or action; and

genomic DNA derived from a patient tissue sample that is further comprised of a label and that contacts the array under conditions wherein hybridization of the genomic DNA and the immobilized nucleic acid polymers are determined by detecting the label at the predetermined position of at the at least two isolated nucleic acid polymers.

18. The platform of claim 17 wherein the at least two isolated nucleic acid polymers are specific for two genes selected from the group consisting of Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Dihydroxyacetone phosphate acyltransferase, Phosphate cytidylyltransferase 1 (choline specific, alpha form), Phosphate cytidylyltransferase 2 (ethanolamine specific), Phosphatidic Acid Phosphatase type 2c, Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase C beta 3 (phosphatidylinositol specific), Phosphatidylinositol-3-Kinase (class2, gamma polypeptide), Choline/ethanolamine phosphotransferase, Lyosphospholipase, Aldehyde dehydrogenase (5 family, member A1), Phospholipase D1 glycosylphosphatidylinositol specific, 1-acylglycerol-3-phosphate acyltransferase, Phosphatidic Acid Phosphate type 2b, Edg 1, Glycerol-3-phosphate dehydrogenase, Sphingosine-1-phosphate lyase 1, Phosphatase and Tenson Homolog (PTEN), Phosphatidic Acid Phosphatase type

2a, Sphingomyelin phosphodiesterase 1, N-acylsphingosine amidohydrolase, Glycerol Kinase, Diacylglycerol Kinase gamma, Acyl-dihydroxyacetone phosphate reductase, Triacylglycerol lipase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

19. The platform of claim 18 wherein at least one of the at least two genes is selected from the group consisting of Phosphatidylinositol-3-kinase (catalytic, alpha polypeptide), Phospholipase D1 (phosphatidylcholine specific), Prostate Differentiation Factor PLAB, Phospholipase A2, Phospholipase D1 glycosylphosphatidylinositol specific, Edg 1, Glycerol-3-phosphate dehydrogenase, EDG 2, EDG 3, EDG 4, EDG 5, EDG 6, and EDG 7.

20. The platform of claim 17 wherein at least one of the isolated nucleic acid polymers is comprised of at least about 19 nucleotides.

21. The platform of claim 17 wherein at least one of the isolated nucleic acid polymers specific for the selected genes is a nucleic acid polymer comprising at least about 19 nucleotides which hybridize under the conditions to a non-coding sequence functionally linked to the coding region of one of the selected genes, wherein the functionally linked sequence is unique to that gene.

22. A physical platform, comprising:

an array of nucleic acid polymers immobilized on a solid support,

wherein the array is comprised of at least two different isolated nucleic acid polymers which are each specific for a different gene directly associated with lipid metabolism, synthesis, or action.

23. A physical platform, comprising:

an array of nucleic acid polymers immobilized on a solid support,

wherein the array is comprised of at least two different isolated nucleic acid polymers which are each specific for a different gene encoding a protein that modifies, oxidizes, reduces, cleaves, binds, or otherwise utilizes bioactive lipids as substrates or ligands.